



RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 10/691,672
Source: IFWP
Date Processed by STIC: 10/18/04

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 4.2 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail. Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom. Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<http://www.uspto.gov/ebc/efs/downloads/documents.htm>), EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box-1450, Alexandria, VA 22313-1450
3. Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 06/05/04):
U.S. Patent and Trademark Office, 220 20th Street S., Customer Window, Mail Stop Sequence, Crystal Plaza Two, Lobby, Room 1B03, Arlington, VA 22202

Revised 05/17/04

Raw Sequence Listing Error Summary

ERROR DETECTED

SUGGESTED CORRECTION

SERIAL NUMBER:

10/691,672

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 Wrapped Nucleics
 Wrapped Aminos The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
- 2 Invalid Line Length The rules require that a line not exceed 72 characters in length. This includes white spaces.
- 3 Misaligned Amino
 Numbering The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use **space characters**, instead.
- 4 Non-ASCII The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.
- 5 Variable Length Sequence(s) contain n's or Xaa's representing more than one residue. **Per Sequence Rules, each n or Xaa can only represent a single residue.** Please present the **maximum** number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
- 6 PatentIn 2.0
 "bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. **This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.**
- 7 Skipped Sequences
 (OLD RULES) Sequence(s) missing. If intentional, please insert the following lines for **each** skipped sequence:
 (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
 (i) **SEQUENCE CHARACTERISTICS:** (Do not insert any subheadings under this heading)
 (xi) **SEQUENCE DESCRIPTION:** SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
 This sequence is intentionally skipped

 Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to **include** the skipped sequences.
- 8 Skipped Sequences
 (NEW RULES) Sequence(s) missing. If intentional, please insert the following lines for **each** skipped sequence.
 <210> sequence id number
 <400> sequence id number
 000
- 9 Use of n's or Xaa's
 (NEW RULES) Use of n's and/or Xaa's have been detected in the Sequence Listing.
 Per 1.823 of Sequence Rules, use of <220>-<223> is **MANDATORY** if n's or Xaa's are present.
 In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 10 Invalid <213>
 Response Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is **required** when <213> response is Unknown or is Artificial Sequence
- 11 Use of <220>

Sequence(s) missing the <220> "Feature" and associated numeric identifiers and responses.
 Use of <220> to <223> is **MANDATORY** if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
 (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
- 12 PatentIn 2.0
 "bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
- 13 Misuse of n/Xaa "n" can only represent a single nucleotide; "Xaa" can only represent a single amino acid



IFWO

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/691,672

DATE: 10/18/2004

TIME: 10:16:19

Input Set : A:\pto.pg.txt

Output Set: N:\CRF4\09282004\J691672.raw

3 <110> APPLICANT: DRUILHE, Pierre
 5 <120> TITLE OF INVENTION: GLURP-MSP3 FUSION PROTEIN, IMMUNOGENIC
 COMPOSITIONS AND MALARIAL VACCINES
 6 CONTAINING IT
 8 <130> FILE REFERENCE: B5768 - AD/VMA/VG
 C--> 10 <140> CURRENT APPLICATION NUMBER: US/10/691,672
 11 <141> CURRENT FILING DATE: 2003-10-24
 13 <160> NUMBER OF SEQ ID NOS: 7
 15 <170> SOFTWARE: PatentIn version 3.1
 17 <210> SEQ ID NO: 1
 18 <211> LENGTH: 491
 19 <212> TYPE: PRT
 20 <213> ORGANISM: P. Falciparum
 22 <220> FEATURE:
 23 <221> NAME/KEY: misc_feature
 24 <222> LOCATION: (1)..(491)
 25 <223> OTHER INFORMATION: GLURP amino acids 24 - 514
 28 <400> SEQUENCE: 1
 30 Lys Thr Asn Thr Ser Glu Asn Arg Asn Lys Arg Ile Gly Gly Pro Lys
 31 1 5 10 15
 34 Leu Arg Gly Asn Val Thr Ser Asn Ile Lys Phe Pro Ser Asp Asn Lys
 35 20 25 30
 38 Gly Lys Ile Ile Arg Gly Ser Asn Asp Lys Leu Asn Lys Asn Ser Glu
 39 35 40 45
 42 Asp Val Leu Glu Gln Ser Glu Lys Ser Leu Val Ser Glu Asn Val Pro
 43 50 55 60
 46 Ser Gly Leu Asp Ile Asp Asp Ile Pro Lys Glu Ser Ile Phe Ile Gln
 47 65 70 75 80
 50 Glu Asp Gln Glu Gly Gln Thr His Ser Glu Leu Asn Pro Glu Thr Ser
 51 85 90 95
 54 Glu His Ser Lys Asp Leu Asn Asn Asn Asp Ser Lys Asn Glu Ser Ser
 55 100 105 110
 58 Asp Ile Ile Ser Val Asn Asn Lys Ser Asn Lys Val Gln Asn His Phe
 59 115 120 125
 62 Glu Ser Leu Ser Asp Leu Glu Leu Leu Glu Asn Ser Ser Gln Asp Asn
 63 130 135 140
 66 Leu Asp Lys Asp Thr Ile Ser Thr Glu Pro Phe Pro Asn Gln Lys His
 67 145 150 155 160
 70 Lys Asp Leu Gln Gln Asp Leu Asn Asp Glu Pro Leu Glu Pro Phe Pro
 71 165 170 175
 74 Thr Gln Ile His Lys Asp Tyr Lys Glu Lys Asn Leu Ile Asn Glu Glu
 75 180 185 190
 78 Asp Ser Glu Pro Phe Pro Arg Gln Lys His Lys Lys Val Asp Asn His
 79 195 200 205

pg 3,5
 Does Not Comply
 Corrected Diskette Needed

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DATE: 10/18/2004

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Input Set : A:\pto.pg.txt

Output Set: N:\CRF4\09282004\J691672.raw

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83      210                      215                      220
86 Gln Gly Ser Leu Lys Leu Lys Ser Phe Asp Glu His Leu Lys Asp Glu
87 225                      230                      235                      240
90 Lys Ile Glu Asn Glu Pro Leu Val His Glu Asn Leu Ser Ile Pro Asn
91      245                      250                      255
94 Asp Pro Ile Glu Gln Ile Leu Asn Gln Pro Glu Gln Glu Thr Asn Ile
95      260                      265                      270
98 Gln Glu Gln Leu Tyr Asn Glu Lys Gln Asn Val Glu Glu Lys Gln Asn
99      275                      280                      285
102 Ser Gln Ile Pro Ser Leu Asp Leu Lys Glu Pro Thr Asn Glu Asp Ile
103      290                      295                      300
106 Leu Pro Asn His Asn Pro Leu Glu Asn Ile Lys Gln Ser Glu Ser Glu
107 305                      310                      315                      320
110 Ile Asn His Val Gln Asp His Ala Leu Pro Lys Glu Asn Ile Ile Asp
111      325                      330                      335
114 Lys Leu Asp Asn Gln Lys Glu His Ile Asp Gln Ser Gln His Asn Ile
115      340                      345                      350
118 Asn Val Leu Gln Glu Asn Asn Ile Asn Asn His Gln Leu Glu Pro Gln
119      355                      360                      365
122 Glu Lys Pro Asn Ile Glu Ser Phe Glu Pro Lys Asn Ile Asp Ser Glu
123      370                      375                      380
126 Ile Ile Leu Pro Glu Asn Val Glu Thr Glu Glu Ile Ile Asp Asp Val
127 385                      390                      395                      400
130 Pro Ser Pro Lys His Ser Asn His Glu Thr Phe Glu Glu Glu Thr Ser
131      405                      410                      415
134 Glu Ser Glu His Glu Glu Ala Val Ser Glu Lys Asn Ala His Glu Thr
135      420                      425                      430
138 Val Glu His Glu Glu Thr Val Ser Gln Glu Ser Asn Pro Glu Lys Ala
139      435                      440                      445
142 Asp Asn Asp Gly Asn Val Ser Gln Asn Ser Asn Asn Glu Leu Asn Glu
143      450                      455                      460
146 Asn Glu Phe Val Glu Ser Glu Lys Ser Glu His Glu Pro Ala Glu Asn
147 465                      470                      475                      480
150 Glu Glu Ser Ser Leu Glu Glu Gly His His Glu
151      485                      490
154 <210> SEQ ID NO: 2
155 <211> LENGTH: 169
156 <212> TYPE: PRT
157 <213> ORGANISM: P. Falciparum
159 <220> FEATURE:
160 <221> NAME/KEY: MISC_FEATURE
161 <222> LOCATION: (1)..(169)
162 <223> OTHER INFORMATION: MSP3 amino acids 212 - 380
165 <400> SEQUENCE: 2
167 Lys Glu Ala Ser Ser Tyr Asp Tyr Ile Leu Gly Trp Glu Phe Gly Gly
168 1                      5                      10                      15
171 Gly Val Pro Glu His Lys Lys Glu Glu Asn Met Leu Ser His Leu Tyr
172      20                      25                      30

```

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Input Set : A:\pto.pg.txt

Output Set: N:\CRF4\09282004\J691672.raw

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175 Val Ser Ser Lys Asp Lys Glu Asn Ile Ser Lys Glu Asn Asp Asp Val
176          35                      40                      45
179 Leu Asp Glu Lys Glu Glu Glu Ala Glu Glu Thr Glu Glu Glu Glu Leu
180          50                      55                      60
183 Glu Glu Lys Asn Glu Glu Glu Thr Glu Ser Glu Ile Ser Glu Asp Glu
184 65          70                      75                      80
187 Glu Glu Glu Glu Glu Glu Lys Glu Glu Asn Glu Lys Lys Lys
188          85                      90                      95
191 Glu Gln Glu Lys Glu Gln Ser Asn Glu Asn Asn Asp Gln Lys Lys Asp
192          100                     105                     110
195 Met Glu Ala Gln Asn Leu Ile Ser Lys Asn Gln Asn Asn Glu Lys
196          115                     120                     125
199 Asn Val Lys Glu Ala Ala Glu Ser Ile Met Lys Thr Leu Ala Gly Leu
200          130                     135                     140
203 Ile Lys Gly Asn Asn Gln Ile Asp Ser Thr Leu Lys Asp Leu Val Glu
204 145          150                     155                     160
207 Glu Leu Ser Lys Tyr Phe Lys Asn His
208          165
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212 <211> LENGTH: 647
213 <212> TYPE: PRT
214 <213> ORGANISM: Artificial Sequence
216 <220> FEATURE:
217 <223> OTHER INFORMATION: protein
219 <220> FEATURE:
220 <221> NAME/KEY: MISC_FEATURE
221 <222> LOCATION: (1)..(647)
222 <223> OTHER INFORMATION: GLURP MSP3 fusion protein
225 <400> SEQUENCE: 3
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228 1          5          10          15
231 Asn Val Thr Ser Asn Ile Lys Phe Pro Ser Asp Asn Lys Gly Lys Ile
232          20          25          30
235 Ile Arg Gly Ser Asn Asp Lys Leu Asn Lys Asn Ser Glu Asp Val Leu
236          35          40          45
239 Glu Gln Ser Glu Lys Ser Leu Val Ser Glu Asn Val Pro Ser Gly Leu
240          50          55          60
243 Asp Ile Asp Asp Ile Pro Lys Glu Ser Ile Phe Ile Gln Glu Asp Gln
244 65          70          75          80
247 Glu Gly Gln Thr His Ser Glu Leu Asn Pro Glu Thr Ser Glu His Ser
248          85          90          95
251 Lys Asp Leu Asn Asn Asn Gly Ser Lys Asn Glu Ser Ser Asp Ile Ile
252          100         105         110
255 Ser Glu Asn Asn Lys Ser Asn Lys Val Gln Asn His Phe Glu Ser Leu
256          115         120         125
259 Ser Asp Leu Glu Leu Leu Glu Asn Ser Ser Gln Asp Asn Leu Asp Lys
260          130         135         140
263 Asp Thr Ile Ser Thr Glu Pro Phe Pro Asn Gln Lys His Lys Asp Leu
264 145          150         155         160

```

This is an insufficient explanation for Artificial Sequence. Give source of genetic material on <223> line.

This would be a sufficient explanation.

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267 Gln Gln Asp Leu Asn Asp Glu Pro Leu Glu Pro Phe Pro Thr Gln Ile
268             165             170             175
271 His Lys Asp Tyr Lys Glu Lys Asn Leu Ile Asn Glu Glu Asp Ser Glu
272             180             185             190
275 Pro Phe Pro Arg Gln Lys His Lys Lys Val Asp Asn His Asn Glu Glu
276             195             200             205
279 Lys Asn Val Phe His Glu Asn Gly Ser Ala Asn Gly Asn Gln Gly Ser
280             210             215             220
283 Leu Lys Leu Lys Ser Phe Asp Glu His Leu Lys Asp Glu Lys Ile Glu
284 225             230             235             240
287 Asn Glu Pro Leu Val His Glu Asn Leu Ser Ile Pro Asn Asp Pro Ile
288             245             250             255
291 Glu Gln Ile Leu Asn Gln Pro Glu Gln Glu Thr Asn Ile Gln Glu Gln
292             260             265             270
295 Leu Tyr Asn Glu Lys Gln Asn Val Glu Glu Lys Gln Asn Ser Gln Ile
296             275             280             285
299 Pro Ser Leu Asp Leu Lys Glu Pro Thr Asn Glu Asp Ile Leu Pro Asn
300             290             295             300
303 His Asn Pro Leu Glu Asn Ile Lys Gln Ser Glu Ser Glu Ile Asn His
304 305             310             315             320
307 Val Gln Asp His Ala Leu Pro Lys Glu Asn Ile Ile Asp Lys Leu Asp
308             325             330             335
311 Asn Gln Lys Glu His Ile Asp Gln Ser Gln His Asn Ile Asn Val Leu
312             340             345             350
315 Gln Glu Asn Asn Ile Asn Asn His Gln Leu Glu Pro Gln Glu Lys Pro
316             355             360             365
319 Asn Ile Glu Ser Phe Glu Pro Lys Asn Ile Asp Ser Glu Ile Ile Leu
320             370             375             380
323 Pro Glu Asn Val Glu Thr Glu Glu Ile Ile Asp Asp Val Pro Ser Pro
324 385             390             395             400
327 Lys His Ser Asn His Glu Thr Phe Glu Glu Glu Thr Ser Glu Ser Glu
328             405             410             415
331 His Glu Glu Ala Val Ser Glu Lys Asn Ala His Glu Thr Val Glu His
332             420             425             430
335 Glu Glu Thr Val Ser Gln Glu Ser Asn Pro Glu Lys Ala Asp Asn Asp
336             435             440             445
339 Gly Asn Val Ser Gln Asn Ser Asn Asn Glu Leu Asn Glu Asn Glu Phe
340             450             455             460
343 Val Glu Ser Glu Lys Ser Glu His Glu Ala Arg Ser Lys Ala Lys Glu
344 465             470             475             480
347 Ala Ser Ser Tyr Asp Tyr Ile Leu Gly Trp Glu Phe Gly Gly Gly Val
348             485             490             495
351 Pro Glu His Lys Lys Glu Glu Asn Met Leu Ser His Leu Tyr Val Ser
352             500             505             510
355 Ser Lys Asp Lys Glu Asn Ile Ser Lys Glu Asn Asp Asp Val Leu Asp
356             515             520             525
359 Glu Lys Glu Glu Glu Ala Glu Glu Thr Glu Glu Glu Leu Glu Glu
360             530             535             540
363 Lys Asn Glu Glu Glu Thr Glu Ser Glu Ile Ser Glu Asp Glu Glu Glu

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Input Set : A:\pto.pg.txt

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364 545 550 555 560
 367 Glu Glu Glu Glu Glu Lys Glu Glu Glu Asn Glu Lys Lys Lys Glu Gln
 368 565 570 575
 371 Glu Lys Glu Gln Ser Asn Glu Asn Asn Asp Gln Lys Lys Asp Met Glu
 372 580 585 590
 375 Ala Gln Asn Leu Ile Ser Lys Asn Gln Asn Asn Asn Glu Lys Asn Val
 376 595 600 605
 379 Lys Glu Ala Ala Glu Ser Ile Met Lys Thr Leu Ala Gly Leu Ile Lys
 380 610 615 620
 383 Gly Asn Asn Gln Ile Asp Ser Thr Leu Lys Asp Leu Val Glu Glu Leu
 384 625 630 635 640
 387 Ser Lys Tyr Phe Lys Asn His
 388 645

391 <210> SEQ ID NO: 4

392 <211> LENGTH: 1941

393 <212> TYPE: DNA

394 <213> ORGANISM: Artificial Sequence

396 <220> FEATURE:

397 <223> OTHER INFORMATION: (DNA)

399 <400> SEQUENCE: 4

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 402 aatataaagt tcccatcaga taacaaagggt aaaattataa gaggttcgaa tgataaactt 120
 404 aataaaaaact ctgaagatgt tttagaacaa agcgaaaaat cgcttggttc agaaaatggt 180
 406 cctagtggat tagatataga tgatatccct aaagaatcta tttttattca agaagatcaa 240
 408 gaaggtcaaa ctcatctctga attaaatcct gaaacatcag aacatagtaa agattttaa 300
 410 aataatgggt caaaaaatga atctagtgt attatttcag aaaataataa atcaataaaa 360
 412 gtacaaaatc attttgaatc attatcagat ttagaattac ttgaaaattc ctcaaacgat 420
 414 aatttagaca aagatacaat ttcaacagaa ccttttcta atcaaaaaca taaagactta 480
 416 caacaagatt taaatgatga acctttagaa ccttttcta cacaaatata taaagattat 540
 418 aaagaaaaaa atttaataaa tgaagaagat tcagaacatc tcccagaca aaagcataaa 600
 420 aaggtagaca atcataatga agaaaaaaac gtatttcattg aaaatgggtc tgcaaatggt 660
 422 aatcaaggaa gtttgaaact taaatcattc gatgaacatt taaaagatga aaaaatagaa 720
 424 aatgaaccac ttgttcattg aaatttatcc ataccaaatg atccaataga acaaatatta 780
 426 aatcaacctg aacaagaaac aaatatccag gaacaattgt ataatgaaaa acaaatggt 840
 428 gaagaaaaac aaaattctca aataccttcg ttagatttaa aagaaccaac aaatgaagat 900
 430 attttaccaa atcataatcc attagaaaat ataaaaacaa gtgaatcaga aataaatcat 960
 432 gtacaagatc atgcgctacc aaaagagaat ataatagaca aacttgataa tcaaaaagaa 1020
 434 cacatcgatc aatcacaaca taatataaat gtattacaag aaaataacat aaacaatcac 1080
 436 caattagaac ctcaagagaa acctaattatt gaatcgtttg aacctaaaaa tatagattca 1140
 438 gaaattattc ttctgaaaa tgttgaaaca gaagaaataa tagatgatgt gccttcccct 1200
 440 aaacattcta accatgaaac atttgaagaa gaaacaagtg aatctgaaca tgaagaagcc 1260
 442 gtatctgaaa aaaatgcccc cgaaactgtc gaacatgaag aaactgtgtc tcaagaaagc 1320
 444 aatcctgaaa aagctgataa tgatggaaat gtatctcaaa acagcaacaa cgaattaaat 1380
 446 gaaaatgaat tcgttgaatc ggaaaaaagc gagcatgaag caagatctaa agcaaaaagaa 1440
 448 gcttctagtt atgattatat tttaggttgg gaatttggag gaggcgttcc agaacacaaa 1500
 450 aaagaagaaa atatgttatc acatttatat gtttcttcaa aggataagga aaatatatct 1560
 452 aaggaaaaatg atgatgtatt agatgagaag gaagaagagg cagaagaaac agaagaagaa 1620
 454 gaacttgaag aaaaaaatga agaagaaaaca gaatcagaaa taagtgaaga tgaagaagaa 1680
 456 gaagaagaag aagaaaagga agaagaaaat gaaaaaaaaa aagaacaaga aaaagaacaa 1740

insufficient explanation -- give source of genetic material
 (see item 11 on Enr summary sheet)

Please correct these types of errors in subsequent sequences.

RAW SEQUENCE LISTING ERROR SUMMARY
PATENT APPLICATION: US/10/691,672

DATE: 10/18/2004
TIME: 10:16:20

Input Set : A:\pto.pg.txt

Output Set: N:\CRF4\09282004\J691672.raw

Invalid Line Length:

The rules require that a line not exceed 72 characters in length. This includes spaces.

Seq#:1; Line(s) 5

VERIFICATION SUMMARY

PATENT APPLICATION: US/10/691,672

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Output Set: N:\CRF4\09282004\J691672.raw

L:10 M:270 C: Current Application Number differs, Replaced Current Application Number